



U.S. Fish & Wildlife Service

Genetic Analysis of Alaskan Coho Salmon

Evidence for population structure at small geographic scales

Introduction

Coho salmon (Figure 1) are one of five species of Pacific salmon found in North America. In Alaska, coho salmon are distributed from the Dixon Entrance in Southeast Alaska, north to Point Hope in the Chukchi Sea, and are the second least abundant species of Pacific salmon. Alaskan coho salmon are found in a variety of freshwater systems, such as large tributaries of the Yukon River and recently de-glaciated coastal streams in Glacier Bay. However, many coho salmon populations occupy small headwater streams with limited spawning and juvenile rearing habitat. These populations are small in size and tend to spawn late in the year (early fall to mid winter) as compared to other Pacific salmon.

Alaska represents half of the North American range for coho salmon. However, information for coho in Alaska is limited. Little is known about their genetic diversity and population structure. It is critical that we obtain this information in order to provide the foundation on which to develop and evaluate conservation and management plans.

Methods

In 1997, the U.S. Fish and Wildlife Service's Alaska Region Conservation Genetics Laboratory (CGL) initiated a genetic study to examine the population structure of Alaskan coho salmon to facilitate conservation and management. The objectives of the study were to estimate and evaluate the degree and spatial distribution of coho population structure.

Fin clips were collected from 50-100 coho salmon from each of 32 putative populations across Alaska (Figures 2 and



Figure 1. Male coho salmon from the Kenai River drainage.

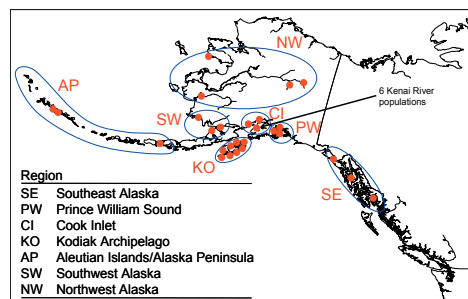


Figure 2. Map of Alaskan coho salmon populations sampled.

3). These samples were genotyped with nine microsatellite DNA markers to estimate population structure within and among 7 geographic regions. Intensive



Figure 3. Collecting fin tissue from a coho salmon. After sampling, fish are returned to the stream to spawn.

sampling in the Kenai River and on the Kodiak Archipelago also allowed for detailed intra-regional analysis.

Population Structure

The degree of population structure in coho salmon was determined by estimating F_{ST} , which is the fraction of the total genetic diversity from all populations due to variation between populations (Figure 4). F_{ST} can be no less than zero (no population structure) and no greater than 1 (completely isolated populations).

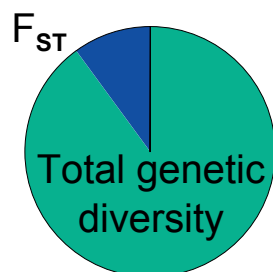


Figure 4. The blue wedge represents an F_{ST} of approximately 0.10 or 10%.

Isolation By Distance

The spatial distribution of population structure was evaluated by testing for genetic isolation by distance (IBD) over all populations and within the Kodiak Archipelago and Kenai River. IBD exists if the genetic distance between populations increases (is correlated) with geographic distance (Figure 5).

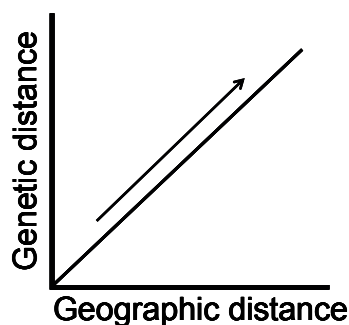


Figure 5. The theoretical relationship between genetic and geographic distance under isolation by distance (IBD).

Results

Our results provide insight into the degree and distribution of genetic diversity in Alaskan coho salmon and have important conservation implications:

First, the results show that the degree of population structure (F_{ST}) is high for all 32 populations (Figure 6), and is as large or larger than that reported for other species of Pacific salmon in Alaska. Coho salmon population structure occurs on a relatively fine geographic scale.

Second, our results indicate that microsatellites have strong potential for use in estimating population contributions for coho salmon in mixed-stock aggregations. In fact, in a collaborative study with the Alaska Department of Fish and Game, we are currently analyzing additional samples from the Kenai River drainage in an attempt to determine the stream of origin for smolt outmigrating to sea.

Finally, our results show that genetic and geographic distances are not correlated at broad geographic scales. Within intensively sampled regions, genetic and geographic distances are correlated for

the Kenai River populations, but not for the Kodiak Archipelago populations. Isolation by distance occurs only at the finest geographic scale and suggests that coho salmon in Alaska are comprised of many small and genetically discrete populations. These results provide an important genetic foundation to guide future studies to precisely define conservation boundaries for Alaskan coho salmon.

Any management or conservation actions affecting coho salmon in Alaska must recognize that their populations are clearly structured at small geographic scales. Activities or conditions that cause declines in abundance are more likely to have strong negative impacts for coho salmon than for species in which genetic variation is distributed over a broader geographic scale (e.g., chum salmon). Coho populations are small, isolated, and contain relatively large amounts of genetic variation. Therefore, they are more susceptible to extirpation and less likely to be augmented or “rescued” by other nearby populations. Every coho population lost represents the loss of significant amounts of genetic variability.

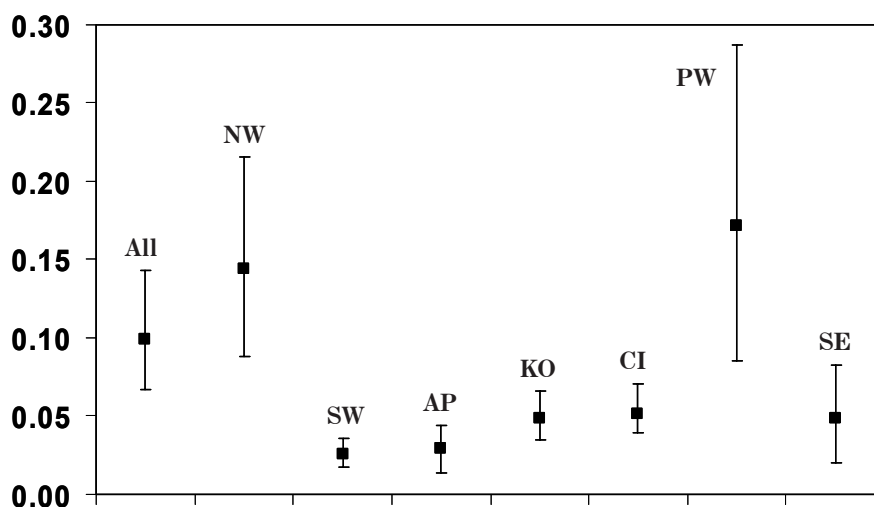


Figure 6. Estimates of the degree of population structure (F_{ST}) for all 32 coho salmon population samples and for population samples from each region. The vertical lines indicate 95% confidence intervals for each estimate.

For complete details see:

Olsen JB, Miller SJ, Spearman WJ, and JK Wenburg (2003) Patterns of intra- and inter-population genetic diversity in Alaskan coho salmon: Implications for conservation. *Conservation Genetics*, In Press.

Genetic data available online at:

<http://www.r7.fws.gov/fish/genelab/home.html>

<http://www.fws.gov>

February 2003

For more information contact:

Jeff Olsen
U.S. Fish and Wildlife Service
Conservation Genetics Laboratory
1011 E. Tudor Road
Anchorage, Alaska 99503
907/786 3598

jeffrey_olsen@fws.gov